

Amendments to the Claims:

This listing of claims will replace all prior versions and listings, of claims in the application:

Listing of Claims:

1. (Currently Amended) A method for selecting [a domestic] an animal for having desired genotypic properties comprising testing said animal for the presence of a parentally imprinted quantitative trait locus (QTL).
2. (Currently Amended) [A] The method according to claim 1, further comprising testing a nucleic acid sample from said animal for the presence of a [parentally imprinted quantitative trait locus (]QTL[)]].
3. (Currently Amended) [A] The method according to claim 1 [or 2]wherein said animal comprises a pig and in [the] said pig said QTL is located at chromosome 2.
4. (Currently Amended) [A] The method according to claim [2 or 3] 1 wherein said animal comprises a pig and in said pig said QTL [is mapping] maps at [around] about position 2p1.7.
5. (Currently Amended) [A] The method according to claim 1 [to 4] wherein said QTL is related to the potential muscle mass and/or fat deposition of said animal.
6. (Currently Amended) [A] The method according to claim 5 wherein said QTL comprises at least a part of an insulin-like growth factor-2 [(IGF2)]gene.

7. (Currently Amended) [A] The method according to [anyone of claims] claim 1 [to 6] wherein said animal comprises a pig and in [the] said pig said QTL comprises a marker characterized as nt241(G-A) or as Swc9[, as identified in figure 4].

8. (Currently Amended) [A] The method according to [anyone of claims 1-7] claim 1 wherein a paternal allele of said QTL is predominantly expressed in said animal.

9. (Currently Amended) [A] The method according to [anyone of claims 1-7] claim 1 wherein a maternal allele of said QTL is predominantly expressed in said animal.

10. (Currently Amended) An isolated and/or recombinant nucleic acid comprising a parentally imprinted quantitative trait locus (QTL) or a functional fragment [derived thereof] of said QTL comprising genetic information capable of influencing a quantitative trait of an animal.

11. (Currently Amended) An isolated and/or recombinant nucleic acid comprising a synthetic parentally imprinted quantitative trait locus (QTL) derived from at least one chromosome or a functional fragment [derived thereof.] of said chromosome comprising genetic information capable of influencing a quantitative trait of an animal.

12. (Currently Amended) [A] The isolated and/or recombinant nucleic acid according to claim 10 [or 11] at least partly derived from a Sus scrofa chromosome.

13. (Currently Amended) [A] The isolated and/or recombinant nucleic acid according to claim 12 wherein said nucleic acid is at least partly derived from a Sus scrofa chromosome 2[, preferably from a region mapping at around position 2p1.7].

14. (Currently Amended) [A] The nucleic acid according to [any one of claims] claim 10 [to 13] wherein said QTL is related to the potential muscle mass and/or fat deposition of said animal.

15. (Currently Amended) [A] The nucleic acid according to [any one of claims] claim 10 [to 14] wherein said QTL comprises at least a part of [a] an insulin-like growth factor-2 [(IGF2)]gene.

16. (Currently Amended) [A] The nucleic acid according to [anyone of claims] claim 10 [to 15] wherein a paternal allele of said QTL is capable of being predominantly expressed.

17. (Currently Amended) [A] The nucleic acid according to [anyone of claims] claim 10 [to 16] wherein a maternal allele of said QTL is capable of being predominantly expressed.

Claims 18-23 (Canceled).

24. (Currently Amended) A transgenic animal comprising the isolated and/or recombinant [a] nucleic acid according to claim 11 [anyone of claims 11 to 16].

25. (Currently Amended) [An animal]The transgenic animal according to [anyone of claims 21-24 which]claim 24 wherein said transgenic animal is a male.

26. (Currently Amended) Sperm or an embryo derived from [an]the transgenic animal according to [anyone of claims 21-25]claim 24.

27. (Currently Amended) [Use of a sperm or an embryo according to claim 26 in] A method for breeding animals destined for slaughter comprising utilizing the sperm or embryo according to claim 26.

28. (New) The isolated and/or recombinant nucleic acid according to claim 13 wherein said isolated and/or recombinant nucleic acid is at least partly derived from a region mapping at about position 2p1.7.

29. (New) The isolated and/or recombinant nucleic acid according to claim 11 at least partly derived from a *Sus scrofa* chromosome.

30. (New) The isolated and/or recombinant nucleic acid according to claim 29 wherein said isolated and/or recombinant nucleic acid is at least partly derived from a *Sus scrofa* chromosome 2.

31. (New) The isolated and/or recombinant nucleic acid according to claim 30 wherein said isolated and/or recombinant nucleic acid is at least partly derived from a region mapping at about position 2p1.7.

32. (New) The isolated and/or recombinant nucleic acid according to claim 11 wherein said QTL is related to the potential muscle mass and/or fat deposition of said animal.

33. (New) The isolated and/or recombinant nucleic acid according to claim 11 wherein said QTL comprises at least a part of an insulin-like growth factor-2 gene.

34. (New) The isolated and/or recombinant nucleic acid according to claim 11 wherein a paternal allele of said QTL is capable of being predominantly expressed.

35. (New) The isolated and/or recombinant nucleic acid according to claim 11 wherein a maternal allele of said QTL is capable of being predominantly expressed.

36. (New) The method according to claim 1 wherein said testing comprises utilizing an isolated and/or recombinant nucleic acid comprising a QTL or a functional fragment of said QTL comprising genetic information capable of influencing a quantitative trait of said animal.

37. (New) The method according to claim 36 wherein said animal comprises a breeding animal or an animal destined for slaughter and wherein said desired genotypic properties further comprise potential phenotypic properties.

38. (New) The method according to claim 37 wherein said desired genotypic properties are related to muscle mass and/or fat deposition.